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☐ 1: Eur J Biochem 2000 Oct;267(20):6140-50

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Cloning, expression and chromosomal localization of a novel human dipeptidyl peptidase (DPP) IV homolog, DPP8.

Abbott CA, Yu DM, Woollatt E, Sutherland GR, McCaughan GW, Gorrell MD.

A. W. Morrow Gastroenterology and Liver Centre, Royal Prince Alfred Hospital, Centenary Institute of Cancer Medicine and Cell Biology and The University of Sydney, NSW, Australia. c.abbott@centenary.usyd.edu.au

Dipeptidyl peptidase (DPP) IV has roles in T-cell costimulation, chemokine biology, type-II diabetes and tumor biology. Fibroblast activation protein (FAP) has been implicated in tumor growth and cirrhosis. Here we describe DPP8, a novel human postproline dipeptidyl aminopeptidase that is homologous to DPPIV and FAP. Northern-blot hybridization showed that the tissue expression of DPP8 mRNA is ubiquitous, similar to that of DPPIV. The DPP8 gene was localized to chromosome 15q22, distinct from a closely related gene at 19p13.3 which we named DPP9. The full-length DPP8 cDNA codes for an 882-amino-acid protein that has about 27% identity and 51% similarity to DPPIV and FAP, but no transmembrane domain and no N-linked or O-linked glycosylation. Western blots and confocal microscopy of transfected COS-7 cells showed DPP8 to be a 100-kDa monomeric protein expressed in the cytoplasm. Purified recombinant DPP8 hydrolyzed the DPPIV substrates Ala-Pro, Arg-Pro and Gly-Pro. Thus recombinant DPP8 shares a postproline dipeptidyl aminopeptidase activity with DPPIV and FAP. DPP8 enzyme activity had a neutral pH optimum consistent with it being nonlysosomal. The similarities between DPP8 and DPPIV in tissue expression pattern and substrates suggests a potential role for DPP8 in T-cell activation and immune function.

MeSH Terms:

- Amino Acid Sequence
- Antigens, CD26/genetics*
- Antigens, CD26/chemistry
- Cell Line
- Chromosome Mapping

- Chromosomes, Human, Pair 15*
- Chromosomes, Human, Pair 19
- Cloning, Molecular
- Growth Substances/chemistry
- Human
- Lymphocytes/enzymology
- Molecular Sequence Data
- Monocytes/enzymology
- Recombinant Proteins/chemistry
- Recombinant Proteins/biosynthesis
- Sequence Alignment
- Sequence Homology, Amino Acid
- Serine Endopeptidases/chemistry
- Support, Non-U.S. Gov't

Substances:

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- Growth Substances

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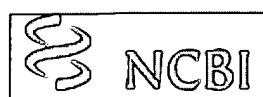
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PMID: 11012666 [PubMed - indexed for MEDLINE]

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☐ 1: AF221634. Homo sapiens dipe...[gi:11095187]

Links

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 AUTHORS Abbott,C.A., Yu,D.M., Woollatt,E., Sutherland,G.R., McCaughan,G.W.
 and Gorrell,M.D.
 TITLE Cloning, expression and chromosomal localization of a novel human
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 JOURNAL Eur. J. Biochem. 267 (20), 6140-6150 (2000)
 MEDLINE 20467194
 PUBMED 11012666
 REFERENCE 2 (bases 1 to 3127)
 AUTHORS Abbott,C.A., Yu,D., McCaughan,G.W. and Gorrell,M.D.
 TITLE Direct Submission
 JOURNAL Submitted (06-JAN-2000) A.W. Morrow Gastroenterology and Liver
 Centre, Centenary Institute of Cell Biology and Cancer Medicine,
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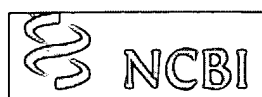
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Links

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 TITLE Cloning, expression and chromosomal localization of a novel human dipeptidyl peptidase (DPP) IV homolog, DPP8
 JOURNAL Eur. J. Biochem. 267 (20), 6140-6150 (2000)
 MEDLINE 20467194
 PUBMED 11012666
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 AUTHORS Abbott,C.A., Yu,D., McCaughan,G.W. and Gorrell,M.D.
 TITLE Direct Submission
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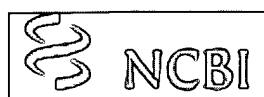
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 AUTHORS Abbott,C.A., Yu,D.M., Woollatt,E., Sutherland,G.R., McCaughan,G.W. and Gorrell,M.D.
 TITLE Cloning, expression and chromosomal localization of a novel human dipeptidyl peptidase (DPP) IV homolog, DPP8
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 TITLE Direct Submission
 JOURNAL Submitted (06-JAN-2000) A.W. Morrow Gastroenterology and Liver Centre, Centenary Institute of Cell Biology and Cancer Medicine, Locked Bag No.6, Newtown, Sydney, NSW 2042, Australia
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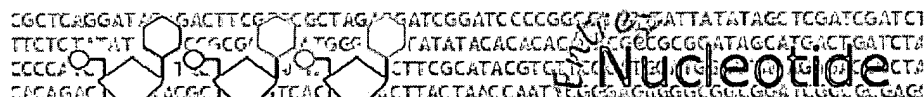
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1081 acgttatatg ggtcacctcg accagaatga acagggtctat tacttaggat ctgtggccat
1141 gcaagcagaa aagttccctt ctgaaccaa tctgttactg ctcttacatg gtttcctgga
1201 tgagaatgtc cttttgcac ataccagtat attactgagt tttttagtga gggctggaaa
1261 gccatatgat ttacagatct atcctcagga gagacacagc ataagagttc ctgaatcggg
1321 agaacattat gaactgcac ttttgacta cttcaagaa aaccttggat cacgtattgc
1381 tgctctaaaa gtgatataat tttgacctgt gtagaactct ctggtataca ctggctattt
1441 aaccaaataa ggaggtttta tcaacagaaa acacagaatt gatcatcaca ttttgatacc
1501 tgccatgtaa catctactcc tgaaaataaa tgtggtgcca tgcaggggtc tacggtttgt
1561 ggtagtaatc taatacctta accccacatg ctcaaatca aatgatacat attcctgaga
1621 gaccagcaa taccataaga attactaaaa aaaaaaaaaa aaaaaaaaaa
```

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Jan 21 2003 18:08:12



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```
/translation="EEDARSAGVATFVLQEEFDRYSGYWCPKAETTPSGGKILRILY
EENDESEVEI IHVTSPMLETRRADSFYRPKTGTANPKVTFKMSEIMIDAEGRIIVDEV
RRLVYFEGTKDSPLEHHLYVVSYNPGEVTRLTDRGYSHSCCISOHCDFFIISKYSNOK
```

NPHCVSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGFTLYGML
YKPHDLQPGKKYPTVLFYGGPQVQLVNNRFGVKYFRLNTLASLGYVVVVIDNRGSC
HRGLKFEGAFKYKMGQIEIDDQVEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALM
QRSDIFRVAIAGAPVTLWIFYDTGYT"

BASE COUNT 312 a 213 c 247 g 311 t
ORIGIN

```
1 ggaagaagat gccagatcag ctggagtcgc tacctttggt ctccaagaag aatttgatag
61 atattctggc tattggtggt gtccaaaagc tgaacaact cccagtgggt gtaaaattct
121 tagaattcta tatgaagaaa atgatgaatc tgaggtggaa attattcatg ttacatcccc
181 tatgttggaa acaaggaggg cagattcatt ccgttatcct aaaacaggta cagcaaattc
241 taaagtcact ttttaagatgt cagaaataat gattgatgct gaaggaagga tcatagttga
301 tgaagtcaga aggctggtat attttgaagg caccaaagac tcccctttag agcatcacct
361 gtacgtagtc agttacgtaa atcctggaga ggtgacaagg ctgactgacc gtggctactc
421 acattcttgc tgcatcagtc agcactgtga cttctttata agtaagtata gtaaccagaa
481 gaatccacac tgtgtgtccc tttacaagct atcaagtcct gaagatgacc caacttgcaa
541 aacaaaggaa ttttgggcca ccattttgga ttcagcaggt cctcttcctg actatactcc
601 tccagaaatt ttctcttttg aaagtactac tggatttaca ttgtatggga tgctctacaa
661 gcctcatgat ctacagcctg gaaagaaata tcctactgtg ctgttcatat atggtggtcc
721 tcaggtgcag ttggtgaata atcggtttaa aggagtcaag tatttccgct tgaataccct
781 agcctctcta gggtatgtgg ttgtagtgat agacaacagg ggatcctgtc accgagggct
841 taaatttgaa ggcgccttta aatataaaat ggggtcaaata gaaattgacg atcaggtgga
901 aggactccaa tatctagctt ctcgatatga tttcattgac ttagatcgtg tgggcatcca
961 cggctggtcc tatggaggat acctctccct gatggcatta atgcagaggt cagatatctt
1021 cagggttgct attgctgggg cccagtcac tctgtggatc ttctatgata caggatacac
1081 gga
```

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Jan 21 2003 18:08:12

[3.4.14.3 Transferred entry: now EC 3.4.19.1 - Acylaminoacyl-peptidase]

3.4.14.4 Dipeptidyl-peptidase III
REACTION: Release of an N-terminal dipeptide from a peptide of four or more residues, with broad specificity
OTHER NAME(S): Dipeptidyl aminopeptidase III; Dipeptidyl arylamidase III; Red cell angiotensinase; Enkephalinase B
COMMENTS: A cytosolic serine-type peptidase active at neutral pH. Highly selective for Arg-Arg-2-naphthylamide at pH 9.2. Inactive on (Glu)₄, (Gly)₄, and tripeptides, as well as bonds involving proline
REFERENCES: 1237, 3197, 4862

3.4.14.5 Dipeptidyl-peptidase IV
REACTION: Release of an N-terminal dipeptide, Xaa-Xbb-Xcc, from a polypeptide, preferentially when Xbb is Pro, provided Xcc is neither Pro nor hydroxyproline
OTHER NAME(S): Dipeptidyl aminopeptidase IV; Xaa-Pro-dipeptidyl-aminopeptidase; Gly-Pro naphthylamidase; Postproline dipeptidyl aminopeptidase IV
COMMENTS: A membrane-bound serine-type peptidase in mammals and flavobacteria
REFERENCES: 2478, 3192, 5345

3.4.14.6 Dipeptidyl-dipeptidase
REACTION: Preferential release of dipeptides from a tetrapeptide, e.g. Ala-Gly-Ala-Gly. Acts more slowly on Ala-Ala-Ala-Ala and Gly-Gly-Gly-Gly
OTHER NAME(S): Dipeptidyl tetrapeptide hydrolase; Dipeptidyl ligase; Tetrapeptide dipeptidase
COMMENTS: A thiol-activated peptidase from cabbage (*Brassica oleracea*). Tetrapeptides are formed from Ala-Ala, Gly-Gly, Ala-Gly and Gly-Ala
REFERENCES: 1253

[3.4.14.7 Deleted entry: Tetralysine endopeptidase]

[3.4.14.8 Transferred entry: now EC 3.4.14.9 - Tripeptidyl-peptidase I and EC 3.4.14.10 - Tripeptidyl-peptidase II]

3.4.14.9 Tripeptidyl-peptidase I
REACTION: Release of an N-terminal tripeptide from a polypeptide
OTHER NAME(S): Tripeptidyl aminopeptidase; Tripeptidyl peptidase
COMMENTS: A lysosomal enzyme active at acidic pH. Inhibited by diisopropyl fluorophosphate. Formerly included in EC 3.4.14.8
REFERENCES: 1111, 3194

3.4.14.10 Tripeptidyl-peptidase II
REACTION: Release of an N-terminal tripeptide from a polypeptide
OTHER NAME(S): Tripeptidyl aminopeptidase; Tripeptidyl peptidase
COMMENTS: A cytosolic enzyme active at neutral pH. Inhibited by diisopropyl fluorophosphate. Formerly included in EC 3.4.14.8
REFERENCES: 275-6, 5066

Title: NOVEL SERINE PROTEASE GENES RELATED TO DPPIV

Inventors: Steve Qi et al.
Attorney Docket No. 70669

DPP4 379 E.....CYRHICYFQIDKK....DCTFITTKGTWEVIG....IEALTSDYLYYISNEYK
DPRP1 473 SKYKRSSSEGLEAPSDFKCPIK....EEIATITSGEWEVLGRHGSNIQVDEVRLVYFEGTK
DPRP2 464 QGYDWSEPFSPGEDEFKCPK....EEIATITSGEWEVLGRHGSNIQVDEVRLVYFEGTK
DPRP3 394 GR.....GEHHIAMLIQSKSEQITVRHITSNWEVTK....IITAYDETTOKIYELSTE

DPP4 424 GMPGGRNLYKIQLSDYTKVTCISCELNPERCONYSVSFSKEAKYIOLRCSGEGIPITLH
DPRP1 529 DSPLEHHLYVVSIVNPGEVTRLIDRCYSHSCCISOHCDEFITSKYSNOKNP.HCVSLYKLS
DPRP2 520 DSPLEHHLYVVSIVNPGEVTRLIDRCYSHSCCISOHCDEFITSKYSNOKNP.HCVSLYKLS
DPRP3 445 SSPRGRQLYSASTEGLLNRQCTISCNFMKEOCTYFDASFSPMNOHFLLECEGERVPMVSLH

DPP4 484 SSVNDKGLRVLEDNSALDKMLQN..VOMPSKKLDFEILNETKFNOMILPHFDKSKKYP
DPRP1 588 SPEDDPTCKTKEFWATILDSAGPLPDYTPPEIFSFESTTGETLYGMLYKPHDLQPGKKYP
DPRP2 579 GPDDPLHNQPRFWASMMEAASCPPDYMPPEIFHHTRSQVRLYGMLYKPHDLQPGKKYP
DPRP3 505 STDNPAKYFLESNSMLKEAILKKKIGKE..EIKILHIDDYELPLQLSLPKDFMDRNOYA

DPP4 542 LHLDVYAGPCSOKADTVFR..LNVATYLASTENIIVASFDRGRSGYOGDKIMHAINRRIG
DPRP1 648 TMLFETGGPOVOLVNNRFKGVKYLRLNTLASLGYMVVVIDNRGSCHRGLNFEAGAKYKMG
DPRP2 639 TMLFVYGGPOVOLVNNRFKGVKYLRLNTLASLGYMVVVIDNRGSCHRGLNFEAGAKYKMG
DPRP3 563 LHLIMDEEPGGOLVTDKEH..IDWDSVLIDMDNVIVAREFDGRSGEGLKILQETERRIG

DPP4 600 TFEEDOMEFAARQFS..KMGFMDNKRITAIWGSYGGYVTSVVLGSGSGVEKCGIAPVVR
DPRP1 708 QTEEDOMEGLQYLASRYDFIDLDRVGIHGWSYGGYLSLMALMORSDFEIVATAGAPVTL
DPRP2 699 QVEEDOMEGLQYFAEKYGFIDLSRVAIHGWSYGGYLSLMGLLHKPOVFNVAIAGAPVTV
DPRP3 621 SVEMKDQITAVKELL..KLPYIDSKRSLINGKGYGGYLASMLKSDKIFKCGSVVAPITTD

DPP4 659 WEYYDSVYTERYMGLPTPEDNLHYNSTVMSRAENFKOVEYLLIHGTADDNVHFQOQSAQ
DPRP1 768 WLENDIGYTERYMGHDPDNEGGYLLGSSVAMQAEKFPSEPNRLLLLHGFLDENVHFAHTSI
DPRP2 759 WMAVDIGYTERYMDVPENNOHGYEAGSVALHVEKLPNEPNRLLLLHGFLDENVHFAHTSI
DPRP3 680 LKLYASAFSERYLGMPSKEES..TYOASVILHNVHGLKEENTLIHGTADTKVHFQHSAE

DPP4 719 ISKALVDVGVDQAMWYTDDEHGLASSTAHQHIYTHMSHFTKOCFSLP.....
DPRP1 828 LLSFLMRACKPYDLQIYPOERHSIRVPESGEHYELHLLHQLQENLGSRIAALKVI.....
DPRP2 819 LNSQLMRACKPYDLQIYPOERHSIRVPESGEHYEVTLLHFLOEYL.....
DPRP3 738 LKHLIRKAGVNTMOMVPEDEGHNVEK.SKYHLYSTILKFEFSDCLKEETSVLPQPEEDE

FIG. 1B

FOOTNOTES 42992660